

IN THE CLAIMS:

Claim 1 (currently amended) An isolated polypeptide comprising ~~the~~ an amino acid ~~sequences~~ sequence selected from the group consisting of SEQ ID NOs; 2, 4, and 6, and fragments thereof.

Claim 2 (original) The isolated polypeptide of Claim 1, wherein the fragments comprise the amino acid residues 60 to 69 of SEQ ID NO.: 2.

Claim 3 (original) The isolated polypeptide of Claim 1, wherein the fragments comprise the amino acid residues 67 to 76 or 72 to 98 of SEQ ID NO: 4.

Claim 4 (original) The isolated polypeptide of Claim 1, wherein the fragments comprise the amino acid residues 451 to 460 or 455 to 472 of SEQ ID NO: 6.

Claim 5 (currently amended) An isolated nucleic acid comprising ~~the~~ a nucleotide sequence selected from the group consisting of SE ID NOs: 1, 3, and 5, and fragments thereof.

Claim 6 (original) The isolated nucleic acid of Claim 5, wherein the fragments comprise nucleotides 253 to 258 of SEQ ID NO: 1.

Claim 7 (original) The isolated nucleic acid of Claim 5, wherein the fragments

comprise nucleotides 273 to 278 of SEQ ID NO: 3.

Claim 8 (original) The isolated nucleic acid of Claim 5, wherein the fragments comprise nucleotides 1424 to 1429 of SEQ ID NO: 5.

Claim 9 (original) An expression vector comprising the nucleic acid of Claim 5.

Claim 10 (original) A host cell transformed with the expression vector of Claim 9.

Claim 11 (currently amended) A method of producing ~~the a~~ polypeptide of ~~Claim 1~~, which comprises the steps of:

- (1) culturing the host cell of Claim 10 under a condition suitable for the expression of the polypeptide; and
- (2) recovering the polypeptide from the host cell culture.

Claim 12 (original) An antibody specifically binding to the polypeptide of Claim 1.

Claim 13 (currently amended) A method for diagnosing ~~the diseases~~ a disease associated with the deficiency of the a SGII gene in a mammal, ~~in particular cancers~~, which comprises detecting the nucleic acid of Claim 5 or ~~the a~~ polypeptide encoded thereby of ~~Claim 1~~.

Claim 14 (currently amended) The method of Claim 13, wherein the detection of the

nucleic acid ~~of Claim 5~~ comprises the steps of:

- (1) extracting total RNA from a sample obtained from the mammal;
  - (2) amplifying the RNA by reverse transcriptase-polymerase chain reaction (RT-PCR) to obtain a cDNA sample;
  - (3) bringing the cDNA sample into contact with the nucleic acid ~~of Claim 5~~;
- and
- (4) detecting whether the cDNA sample hybridizes with the nucleic acid ~~of Claim 5~~.

Claim 15 (original) The method of Claim 14, further comprising the step of determining the amount of the hybridized sample.

Claim 16 (currently amended) The method of Claim 13, wherein the detection of the nucleic acid ~~of Claim 5~~ comprises the steps of:

- (1) extracting the total RNAs of cells obtained from the mammal;
- (2) amplifying the RNA by reverse transcriptase-polymerase chain reaction (RT-PCR) with a set of primers to obtain a cDNA comprising the fragments comprising nucleotides 253 to 258 of SEQ ID NO: 1 or nucleotides 273 to 278 of SEQ ID NO: 3 or nucleotides 1424 to 1429 of SEQ ID NO: 5; and
- (3) detecting whether the cDNA is obtained.

Claim 17 (currently amended) The method of Claim 13, wherein the detection of the nucleic acid ~~of Claim 5~~ comprises the steps of:

- (1) extracting the total RNAs of cells obtained from the mammal;
- (2) amplifying the RNA by reverse transcriptase-polymerase chain reaction (RT-PCR) with a set of primers to obtain a cDNA comprising the fragments comprising nucleotides 240 to 269 of SEQ ID NO: 1 or nucleotides 261 to 290 of SEQ ID NO: 3 or nucleotides 1413 to 1442 of SEQ ID NO: 5; and
- (3) detecting whether the cDNA is obtained.

Claim 18 (original) The method of Claim 16, wherein the forward primer has a sequence comprising the nucleotides 253 to 258 of SEQ ID NO: 1 and the reverse primer has a sequence complementary to the nucleotides of SEQ ID NO: 1 at any other locations downstream of nucleotide 258, or alternatively, the reverse primer has a sequence complementary to the nucleotides of SEQ ID NO: 1 containing nucleotides 253 to 258 and the forward primer has a sequence comprising the nucleotides of SEQ ID NO: 1 at any other locations upstream of nucleotide 253.

Claim 19 (original) The method of Claim 17, wherein the forward primer has a sequence comprising the nucleotides 240 to 269 of SEQ ID NO: 1 and the reverse primer has a sequence complementary to the nucleotides of SEQ ID NO: 1 at any other locations downstream of nucleotide 269, or alternatively, the reverse primer has a sequence complementary to the nucleotides of SEQ ID NO: 1 containing nucleotides 240 to 269 and the forward primer has a sequence comprising the nucleotides of SEQ ID NO: 1 at any other locations upstream of nucleotide 240.

Claim 20 (original) The method of Claim 16, wherein the forward primer has a sequence comprising the nucleotides 273 to 278 of SEQ ID NO: 3 and the reverse primer has a sequence complementary to the sequence complementary to the nucleotides of SEQ ID NO: 3 at any other locations downstream of nucleotide 278, or alternatively, the reverse primer has a sequence complementary to the nucleotides of SEQ ID NO: 3 containing nucleotides 273 to 278 and the forward primer has a sequence comprising the nucleotides of SEQ ID NO: 3 at any other locations upstream of nucleotide 273.

Claim 21 (original) The method of Claim 17, wherein the forward primer has a sequence comprising the nucleotides 261 to 290 of SEQ ID NO: 3 and the reverse primer has a sequence complementary to the sequence complementary to the nucleotides of SEQ ID NO: 3 at any other locations downstream of nucleotide 290, or alternatively, the reverse primer has a sequence complementary to the nucleotides of SEQ ID NO: 3 containing nucleotides 261 to 290 and the forward primer has a sequence comprising the nucleotides of SEQ ID NO: 3 at any other locations upstream of nucleotide 261.

Claim 22 (original) The method of Claim 16, wherein the forward primer has a sequence comprising the nucleotides 1424 to 1429 of SEQ ID NO: 5 and the reverse primer has a sequence complementary to the nucleotides of SEQ ID NO: 5 at any other locations downstream of nucleotide 1429, or alternatively, the reverse primer has a sequence complementary to the nucleotides of SEQ ID NO: 5 containing nucleotides 1424 to 1429 and the forward primer has a sequence comprising the nucleotides of SEQ ID NO: 5 at any other locations upstream of nucleotide 1424.

Claim 23 (original) The method of Claim 17, wherein the forward primer has a sequence comprising the nucleotides 1413 to 1442 of SEQ ID NO: 5 and

the reverse primer has a sequence complementary to the nucleotides of SEQ ID NO: 5 at any other locations downstream of nucleotide 1442, or alternatively, the reverse primer has a sequence complementary to the nucleotides of SEQ ID NO: 5 containing nucleotides 1413 to 1442 and the forward primer has a sequence comprising the nucleotides of SEQ ID NO: 5 at any other locations upstream of nucleotide 1413.

Claim 24 (original) The method of Claim 16, wherein the forward primer has a sequence comprising the nucleotides of SEQ ID NO: 1 at any other locations upstream of nucleotide 253 and the reverse primer has a sequence complementary to the nucleotides of SEQ ID NO: 1 at any other locations downstream of nucleotide 258.

Claim 25 (original) The method of Claim 16, wherein the forward primer has a sequence comprising the nucleotides of SEQ ID NO: 3 at any other locations upstream of nucleotide 273 and the reverse primer has a sequence complementary to the nucleotides of SEQ ID NO: 3 at any other locations downstream of nucleotide 278.

Claim 26 (original) The method of Claim 16, wherein the forward primer has a sequence the nucleotides of SEQ ID NO: 5 at any other locations upstream of nucleotide 1424 and the reverse primer has a sequence complementary to the nucleotides of SEQ ID NO: 5 at any other locations downstream of nucleotide 1429.

Claim 27 (original) The method of Claim 24, the cDNA sample amplified from SEQ ID NO: 1 is 339bp shorter than that from SGII.

Claim 28 (original) The method of Claim 25, the cDNA sample amplified from SEQ ID NO: 3 is 259bp shorter than that from SGII.

Claim 29 (original) The method of Claim 26, the cDNA sample amplified from SEQ ID NO: 5 is 533bp shorter than that from SGII.

Claim 30 (original) The method of Claim 16, further comprising the step of detecting the amount of the amplified cDNA sample.

Claim 31 (currently amended) The method of Claim 13, wherein the detection of the polypeptide ~~of Claim 1~~ comprises the steps of contacting ~~the~~ a antibody that specifically binds to the polypeptide of Claim 12, with protein samples extracted from the mammal, and detecting whether an antibody-polypeptide complex is formed.

Claim 32 (original) The method of Claim 31, further comprising the step of determining the amount of the antibody-polypeptide complex.